

EXHIBIT 5

AGGTGGGAC TCAATGCTTA GGCCTCTTA GAGTGTGGG GTGGAGCGAT TAGGATGCTG GGCCTTAGT GTGGGCGAG CACATGTGAC TGACAAAC AGAATTCAGG AAGAGCTCC 1700
 AGGAAGAGT GTGGGTGAC CTAAGTGGG GACTECCACA GCACAGTGT AGGTGTGA GTCCACCTC CAGCAGCTG TCAGCACCAC TGCCCTCCCG TCCACCTCA CAAGAGGGG ACCTAAGAC 1830
 CACCTGCTT CACCACTAC CTCTGTGT GTGTGACCA ACCTACTTC TGTCACATA AATGCTGTA CACTGTGCT CACATCAAG GGAGAAATC TGAITGTCA GGGGTGCGA 1960
 AGACAGGTC TGTGTCTAT TTGTCTAGG GTAGAGTCC TTGGAGTCC CAGAGTCTC CCAAGCTAG TGGGTGAGG TTGTAGCG GGTGTGCG CTGAGACAG GCTCAGACC 2090
 GCTGTGCCC TGGGATGCT TTGAGTCCC AGGACTTGA AATGTGAC GCTTGGGCC CTTCCAGG CATCAGGA TGTCTTCC TGAGGCTTT CAGGACGA GACCTCTGG CTTGACCTC 2220
 CTTGTGCT CAGCTTCC CTTCTGACT GGACCCCAT CTTGAGTCC ATCCACCA CTTCTTCC CAGTGGCT CTGCGACAC ACCACGTA CTTTCTGAG GCAATATCT GATCAGATCA 2350
 AGTCCGACC GGTCTCCAC CTACCATG GTCTCTAG GTCCTGAG TGGCTGCG CTTCTGAG AGCAGGATC AGGCAAGG CAGTGGCTC AAGTGGCT GGTGGTCTT GGACAGCAG 2480
 CAGCCGACC AGCAGAAC CTGTACTG GTTAGAGC CAGACCTCT GGCCTCATC TCCCACTCT CAATACTT CAGGAGG AGGCGCAT CTTAGGGT CCCCAGGC CCGCAGCAG 2610
 AGGAGTGT GGAAGTGA GAGGCGGAG TGAATGTTG AGGATTTGG GTCTTTGCA TGAAGAGCT GTGTGGAG GGAACATG CAGAGACG ACTGAGCTG CATGGGAGA GGGTGTGCT 2740
 CCAAGGACT GGGATGAGG CTGGGCGCG CTGAGGGCG GGGAGGGCG AGGAGGACC AGCTCTAGC AGCCACGAC CATGGGCTT CGATCTGT TTGTCTGAA GCTCTCTCT 2870

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CCCCCTCCCG CTCACCCGT GCTCTGCCC ACCCGGCGC GCGCTCCCG ACACGGCTG CAGAGGCTG AGCTGCCCC CTTCTCTCCG AGCTG GCT TTC TGG TCC AAG CAC GTC GCTCAGT 2993
 GCGTTCTAGA TCCCGGCTG CACTACCGC GCGCGGCCC CTGGGATCT CTGGGCGCTG ACCCTTACC CCGCTTGTG TCGCAGT AC GGT CAC CAG TGC TTT GTC CCC TTG GAG 3111
 His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg 91
 CAC CCG TGC GCC AGC CTG TGC TGC GGC CAC GGC ACG TGC ATC GGC ATC GGC TGC AGC TGC GGC TGC GGC TGC GGC TGC GGC TGC GGC TGC GGC TGC GGC 3216
 G TGTGAGG GAGAGGTG ATGCTGGCG GCGCGGCGC GGGGCTGGG CCGGTTGGG GCGCGGCGC CAGACAGC TCCCGGCGC CTCCCTGCG CCGAGT AG GTG AGC TTC CTC AAT 3336

46

Cys His Pro Ala
 TGT CAC CCC GCA G TGTGAGGCG CCAATACAT CCGCCAGGA TACGCTGGG TCGGGGTGG CAGCGGCGC CACGCGGCG CTGAGAGG TTCTAGGA GGGAGGAG 3564
 AACAGATG AGCTTGGGG CAGCGGACA CCGCGGCA ACAGGCGCA CTGTAGCG GAGTGGG GAGCTGCG GCGCTCCG CTCTCTCTT CTCTGCTCC CCGCTCTCTC 3694
 CCGCGGCCC TGGAGCTGG GCGCCTCC TGGAGGCGA GCGAGTGT GGTTCGCT CCGAGTCA GCGTATGG GCGAGGCT CCGCTCTG CCGCTCTG CCGCTCTG GCTTTCTCT 3824
 GAGCTGCC GCGGTGAT CATTCTCT CTTACCCC TTGCTCTT GAGGAGAA CAGATCCG ATTCTCTT CTCTATAT TCTCTTTA TCGATTAA TCAATTTAT ATATGATGA 3954
 AACTTAAA ATCAGAGTTT TACACTTT ACCTTTGAG CATGCTGTT CTGGGATG GCTTTTTT CATTATTT CATATAGT GAGCCCTTT AATGAGAA TTCTATCTT CTGCTCTAG 4084
 GCGATTATC ACTATTTCT TCTATCTT CCGCTTACT TCTCTTCT GAGCTCTG TTGCTGAG CTGAGTGA ATGAGTGT CTAGCTAC CAGACCTCC GCTCTCTG TTGCTCTG 4214
 TGTCTCTT CAGGAGCT TCTTTTTT CTTTTTTT CAGATGAGT TCTACTTG TTGCTGAG TTGCTGAG TTGCTGAG TTGCTGAG TTGCTGAG TTGCTGAG TTGCTGAG 4344
 TCTCTGCG CAGCTCCG AGAGTGGG ATTACAGCA TCGCCGCA CCGCTCTG ATTCTGTT TTGTAGAG AGGGGTTT TCGCTGG TCAAGTGT CTGCTCTG TCACTGAG 4472
 TGACTACT GCTTGGCT CCAAGTGC TGGATAGA GGTGAGC AGCGGCA GCTCTTCA GGAATTT TCAACTTT TATCTCAT CTCTGAGA AATATTTT TGGCAGCT 4604
 CAGTACTA GACCAATAT TCCAGACT TGGAGGCT AGGTGGAG ATTCTGAG TTGAGGTT TGAATAG CTTGGGAA CAGTACAG CCGCTCTG CCGCTCTG TGGCAGCT 4734
 GATCTAAA TTTCTTTT TATTTGAA TATATAGA TTCTAGAA GTCTGAGA AATCTGCT GCGCTGTT GCGCTGTT GCGCTGTT TTTTAAAA AGTAAAAA 4864
 CCAAGTGG AGGCTGTT TTTTGGCT TTCTTAAA GAGCTCTC AGCTCTGG AGATGGAG ACCTTACC ATGGTCTG GCGCTGAG CAGGCTGG GAGGCGAG TGGTCTCT 4994
 CAGATGCT GCAATTTGA TGTCTCTG TGGTCTGA AGACACAC TCTCTCTG AGCGGCTC CAGTCTCA CAGTCTCA CAGTCTCA CAGTCTCA CAGTCTCA CAGTCTCA 5124
 AGAGGAG GCTTTGCG TTCTCTTA AACTCTAA CATGCTCC CCGCTGCT GCGCTGCT AGCGGCA CCGCTGCT GCGCTGCT AGCTCTCC AGCTCTCC AGCTCTCC 5254
 AGGCTGAG ATTCTGCT TCTGCTGC CAGTCTGT ACTGCTCA TCACTGCT GCACTTCT GGAATTTG CTTGTTG TTGTTG TTGTTG TTGTTG TTGTTG TTGTTG 5384
 AGCTCCAT GCTCTTTA GCTAGAT CTGAGTGG CATTAGG CAGTCTGG CTGACTTC AGCTCTCT CTGACTTC CTGACTTC CTGACTTC CTGACTTC CTGACTTC 5514

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Cys Ser Leu Asp Asn Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Cys Ser Cys Ala Pro Gly Tyr Leu Gly Asp Asp Leu Leu Gln 136
 TGC TCT CTG GAC AAC GGC GGC TGC ACG CAT TAC TGC CTA GAG GAG GTG GGC TGG CCG CCG TGT AGC TGT GCG CCG TAC AAG CTG GGG CAC GAC CTC CTG CAG 3440

92

Glu Val Ser Phe Leu Asn
 G TGTGAGG GAGAGGTG ATGCTGGCG GCGCGGCGC GGGGCTGGG CCGGTTGGG GCGCGGCGC CAGACAGC TCCCGGCGC CTCCCTGCG CCGAGT AG GTG AGC TTC CTC AAT 3336

FIG. 2 CONT.

CACAAATG CCAATGCTAT TGTAGGAGT CTTCAAGAT GCTACCTCC TCTCTCTGT ANTCTCTT CTTCTGAGG ACCTACAG CATECCATTA TGAGACCTTA CTAATCCAG GGAATACCC 5644
 CAAAGGCT GGGATACAT CACCTATGA AGGACACA GGGAGTGGG CATCTGCT GGGCTACTG TTGCTACTG GGGTACTG ACTGACTGAC 5774
 TGTCTGAG GGGTTGTA TTGTATC AGGATAC CCAACAGC CTGGGTAA TTGAGCTTC AGAGCTTT TTAGACACA CAGCCAGTG GAGATGCG TTGCTCTAG 5904
 TCTGCAAT CAGTGGACT GTTTGTGAC TGACTACTG ACTGCTGGG TGACTGGAG GGTTCATAG CTAATATTA TGGAGTGTG TAAGTATAT TGGTCTCTG AACCTGAC TGTGCAAG 6034
 137
 TGGCCACAG GCTGGAGAG CACCAAGCA GGGGGCAGT CTGGGAGGA GTGCCGGGA GGGCCCTEAC CACCTCTCC TACCCTAC TG AAG TTC CCT TGT GGG AGG CCC TGG AAG CGG 6154
 Met Glu Lys Lys Arg Ser His Leu Val Lys Arg Asp Thr Glu Asp Glu Val Asp Pro Arg¹⁸⁴ Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
 ATG CAG AAG AAG CGC AGT CAC CTG AAA CGA GAC ACA GAA CAA GAA CAA GAA GTA GAT CCG CGG CTC ATT GAT GGG AAG ATG ACC AGG CGG GGA GAC AGC CCC 6259
 184
 Trp Glu
 TGG CAG TGGGAGGCG AGGCAGCACC GGTCTGTAC GTGCTGGGTC GGGATCACT GATTCATCC TGGCAGCTAT GCTCAGGGTG CAGAACCCA GGGGAGGCG CTGCCATTC GTTGGGGGA 6385
 TGAATAGT GGGGATGCT TCAGGGAAG ATGACGCA CCGTAGGGA CAGGTCGCT GAGGGAGG GATGGAGGCT CTGCAGGAGG CAGGTTACA GTTCTAATA 6515
 AGAGTGA AGACATGCT TCTGTGGCG GATTTAGG AGAGCTTG ATGAGCTTG AGGGAGGCG GGGCTAGTA CCCCCTCAGG CTTCCATG GAACTGAC TTAATGGGT 6645
 CCCCCTCG CAGGATG GGGAGATGG AACCAAG TGGAGTAT TGGCTGGG ACTCAGCTC TGAAGGCTC AGGACCCCA AGACCCGGA GGGCAGTGG ACCACAGA GGAAGGCT 6775
 TGAATAGG GGTAGGA GGGCAGG AGATCCAG CAGCTGGG GGCANAGT CTCTCGAA CACACAGG CTGCCAGG TCTAGGATG AGAGAGCTC GTGGGGCAT GTTGTGTG 6905
 CTGAGGTGA CTGAACAT ATGAACATG CAGCAAGC ATGGCAAG GAGGAGAC ACCTGGGAC TGTAAATG GCAAAATG AAACCCGAG AAGGCTAA GCTATGCC 7035
 185
 ATATGACC GGAACCCAG AAGTGCTA TGAACCCAG GTGCCCTGA CTGGAGGTG TCAGGAGGA GGGCTGTAT GTCATCTC CACCCCTTC CAG Val Val Leu Leu Asp Ser Lys 7159
 Lys Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu 223
 AAG AAG CTG GCC TGC GGG GCA GTG CTC ATC CAC CCC TCC TGG GTG CTG ACA GCG GCC CAC TGC ATG CAT CAG TCC AAG AAG CTC CTT GTC AGG CTT G GTATGGCTG 7266
 CAGCCAGCA GAAGGGGCT GCCAGAGGCT TGGTAGGCG GACAGGCG GCTGTTCAGG TTGGGGGAC CCGCTCCCG AGGTGCTTA GCAAGAGCT TCTTAGCTC CACAGAGGT GTTGGGGCG 7396
 AAGAGCTA TGTGCCCA CCGTCCAC CCAATATTT CCAATATTT GAGTAGGG GTTCTGTGT GGGCTCTG AATCTGGA CAGTACCTC CACACATG TTGTGAGG GCTACACAGA 7526
 CCTTACCT TCATCTCA CTATGAGA GAGGCTGT TGGCTCTG CACCTTGG TCAGAGAC AGCAGGCT GGGCTAGG CTGTGCTTC CACACTGA CAGGATGA GCTGTACAGA 7656
 GGAAGCTA GATCTGCA AGCCACAG GTGCTTCT AGAGGCTG GGGTCTTAT GCAATGGCC GATCTATGG CAATCTCTG AGGGGGGT TGGCTACT CTATTGCA AAGAGAGC 7786
 AAGATAT GAGAGGCG AATTCATAT TCTACAG ATAATCTATG CCAAGTCTG CAGTGGCTT GCTTAGAT TCCAGGTC TCTTCCAG GAACTACAG TCTGACTGA CAGGCTCTC 7916
 TCTTCAAG GGAACCGG CTGTCTCC CTGGAGTGC GGTGTCTG GGGTCTCT CAGTGGCTT CAGTGGCTT TGGTCTCT GGGTCTCT TCTTGTG GCTGTGCTG 8046
 TGTCTGGGT TTTCCAGGCT CCGGGCTC CTTGCTCC ATCTCTCT TGGTCTCAG GCTCTGAC TCTGAAAC CACAGCAT CCACTCTT TGGATGCA CCGTGGCC ACTCTCTG 8176
 GAGGAAAG TCACTGTTA TGGGTCTA GGCAGTGC AGGTGGCTC GGGCAGTGC TGGGAGGTG GTCTGGA GGTCTGGGT CAACCTCTT CAGGCTCTT CCGGCTCT CAGGGGCA 8306
 224
 GAGTGGGT GGGCTCAGA AAGTGCAAT GGGGAGG TCCCGGAG CCACTCTGAC TGTGCTCT GGGCTCTT CA GAG TAT GAC CTG CGG CGC TGG GAG AAG TGG GAG CTG GAC 8426
 Leu Asp Ile Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His Leu Ala Glu Pro Ala Thr Leu Ser Glu Thr
 CTG CAC ATC AAG CAG GTC TTC GTC CAC CAC AAC TAC AGC AAG AGC ACC CAC CAC AAT CAC ATC GCA CTG CTC GCG CAG CCC ACC CTC TCG CAG ACC 8531

FIG. 2 CONT.

FIG. 3

-42 -40 -30
 Het Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr
 CCG CCA ACT TCC ACT ATC TCC ACC ACC CCC CCC TGT CCC ACT CCC TCC ACA ATC TCG CAG CTC ACA ACC CTC CTC CTC TTC CTC CCC ACC 39

-20 -10 -1 +1
 Trp Gly Ile Ser Gly Thr Pro Ala Pro Leu Asp Ser Ser Ser Val Phe Ser Ser Ser Glu Arg Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala
 TCG CGA ATT TCC GCC ACA CCA CCT CCT CTT GAC TCA CTC TTC TCC ACC ACC CAG CGT GCC CAG CAG GTG CTG CGG ATC CGC AAA CGT GCC 129

10 20 30
 Asn Ser Phe Leu Glu Glu Leu Arg His Ser Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys Asp Phe Glu Glu Ala Lys Glu Ile Phe
 AAC TCC TTC CTG CAG CAG CTC CCT CAC CAC ACC ACC CTG CAG CGG GAG TCC ATA CAG CAG ATC TGT CAC TTC CAG CAG CGC AAG GAA ATT TTC 219

40 50 60
 Gln Asn Val Asp Asp Thr Leu Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro Leu Glu His Pro Cys Ala Ser
 CAA AAT CTC CAT CAC ACA CTG CCC TTC TCC TCC TCC TCC CAC CAC CCT CAC CAC TCC TTC CTC TTC CCC TTC CAG CAC CGC TCC CCC ACC 309

70 80 90
 Leu Cys Cys Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg
 CTG TCC TCC CGG CAC CGC ACG TCC ATC CAC CAC CCC ATC CCC ACC TTC ACC TCC CAC TCC CGC ACC CGC TCG CAG CGC CCC TTC TCC CAG CGC 399

100 110 120
 Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys Ser Cys Ala
 CAG CTG ACC TTC CTC AAT TCC TCT CTC CAG CAC AAC CAC CAC CCG CCC TCC ACC CAT TAC TCC CTA CAG CAG CTC CGC TCG CGC CCC TGT ACC TGT CGC 489

130 140 150
 Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys Lys
 CCT CGC TAG AAG CTG CGG GAG CAC CTC CTC CAG TGT CAC CCC CCA CTC CAC TCT CCT TCT CGC ACC CGC TCG AAG CGC ATC CAC AAG AAG 579

160 170 180
 Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser
 CCC ACT CAC CTC AAA CCA CAC ACA CAA CAC CAA CAA CAT CCG CGC CTC ATT CAT CGC AAG ATC ACC ACC CGC CCA CAC ACC 669

190	200	210	
Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His			759
CCC TGG CAG CTC CTC CAG TCA AAG AAG AAG CAG TCC GCG GCA CTC ATC CAC CCC TCC TGG CTC CAC ACA CCG CCC CAC			
220	230	240	
Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu Glu Tyr Asp Leu Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys			849
TCC ATG CAG CAG TCC AAG AAG CAG CTC CTT GTC ACG CTT GCA CAG TAT CAC CTC GCG CCG TGG CAG AAG TGG CAG CTC CAG CTC AAT AAG			
250	260	270	
Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln			939
GAG CTC TTC CTC CAG CCC AAG TAC AAG AAG AAG ACC ACC CAC AAT CAC ATC GCA CTC CTC CAG CTC CAG CCC CAG CCC ACC CTC TCC CAG			
280	290	300	
Thr Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu Thr Leu Val Thr Gly Trp Gly			1029
ACC ATA CTC CCC ATC TCC CTC CCC CAG ACC AAG CCG CTT GCA CAG CCG CAG CAG ACC CTC CTC GTG ACC GCG TCC CCC			
310	320	330	
Tyr His Ser Ser Arg Glu Lys Glu Ala Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val Pro His Asn Glu Cys			1119
TAC CAC ACC ACC CCA CAG CAG CAG CCC AAG ACA AAG ACC TTC CTC CTC AAC TTC ATC AAG ATT CCC CTC CCG CAC AAT CAG TCC			
340	350	360	
Ser Glu Val Met Ser Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly Asp Ser Gly			1209
ACC CAG CTC ATC ACC AAC ATC CTC TCT CAG AAC ATG CAG TCT GGT TGT GCG GCG ATC CTC CCC CAG CCG CAG CAT CCC TCC CAG CCC CAG ACT CCG			
370	380	390	
Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Cys Gly Leu Leu His Asn Tyr Gly			1299
GCG CCC ATC CTC GCG TCC TTC CAG GCG ACC TCC TTC CTC CTC GCG CTC AGC TGG GGT GAG GCG TGT GCG CTC CTT CAC AAC TAC CCC			
400	410	419	
Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro STOP			1389
GTT TAC ACC AAA CTC ACC CCG TAC CTC CAG TCG ATC CAT CCG CAC ATC ACA CAG AAC GAA CCC CCC CAG AAG ACC TGG GCA CCT TAG CCA			

FIG. 3 CONT.